

RAW SEQUENCE LISTING

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Application Serial Number: 10/524,983
Source: IFWP
Date Processed by STIC: 08/09/2006

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IFWP

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DATE: 08/09/2006

PATENT APPLICATION: US/10/524,983

TIME: 09:32:12

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4 <110> APPLICANT: ALBANG, Richard
 5 FOLKERS, Ulrike
 6 FRITZ, Andreas
 7 GERHARD, Beatrix
 8 HEINRICH, Oliver
 9 ILGENFRITZ, Hilmar
 10 MAIER, Dieter
 11 SPREAFICO, Fabio
 12 WAGNER, Christian
 13 DE BOER, Lex
 14 MEIMA, Roelf Bernhard
 16 <120> TITLE OF INVENTION: NOVEL LIPASES AND USES THEREOF
 18 <130> FILE REFERENCE: 246152025100
 20 <140> CURRENT APPLICATION NUMBER: US 10/524,983
 C--> 21 <141> **CURRENT FILING DATE: 2005-02-18**
 23 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/009145
 24 <151> PRIOR FILING DATE: 2003-08-15
 26 <150> PRIOR APPLICATION NUMBER: EP 02102168.8
 27 <151> PRIOR FILING DATE: 2002-08-19
 29 <150> PRIOR APPLICATION NUMBER: EP 02102169.6
 30 <151> PRIOR FILING DATE: 2002-08-19
 32 <150> PRIOR APPLICATION NUMBER: EP 02102170.4
 33 <151> PRIOR FILING DATE: 2002-08-19
 35 <150> PRIOR APPLICATION NUMBER: EP 02102171.2
 36 <151> PRIOR FILING DATE: 2002-08-19
 38 <150> PRIOR APPLICATION NUMBER: EP 02102172.0
 39 <151> PRIOR FILING DATE: 2002-08-19
 41 <150> PRIOR APPLICATION NUMBER: EP 02102173.8
 42 <151> PRIOR FILING DATE: 2002-08-19
 44 <150> PRIOR APPLICATION NUMBER: EP 02102174.6
 45 <151> PRIOR FILING DATE: 2002-08-19
 47 <150> PRIOR APPLICATION NUMBER: EP 02102176.1
 48 <151> PRIOR FILING DATE: 2002-08-19
 50 <150> PRIOR APPLICATION NUMBER: EP 02102178.7
 51 <151> PRIOR FILING DATE: 2002-08-19
 53 <150> PRIOR APPLICATION NUMBER: EP 02102179.5
 54 <151> PRIOR FILING DATE: 2002-08-19
 56 <150> PRIOR APPLICATION NUMBER: EP 02102181.1
 57 <151> PRIOR FILING DATE: 2002-08-19
 59 <150> PRIOR APPLICATION NUMBER: EP 02102183.7
 60 <151> PRIOR FILING DATE: 2002-08-19
 62 <160> NUMBER OF SEQ ID NOS: 39
 64 <170> SOFTWARE: PatentIn version 3.1

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68 <212> TYPE: DNA
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74 aggtatttaa ctttgggcga taccaactac gcgtgcactt tgaagcatag cacggcgcgc      180
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80 tgctctatat ccgagacaaa ccacaactta ttcaatttaa gcccgagtcc ataactatcc      540
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114 ccgaagcgat ccagcagttg atgggtgagc cccccccccc ccccttccc accaatcccc      2580
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118 ctacgagtcg atggcggggc atctgtgcat gggtgtcccg aggagggttc tcagtcagaa 2820
119 gatgaaggag tatgaggagc aagtgtttgc gtatcgggtg gatgtcgtcg cgttgaatga 2880
120 ttcgagtacg attgggggtg cgcattttgc tgaggtaatg ccatccatcc atcccctatt 2940
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125 gcgtgtgggt ctaatgaggg tgacagtctc tggatatccc cactggccga aatacaacct 3240
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128 gtagtactac tatatgtata taggagggtg tgggtgaaaa gtagatagta gtactatata 3420
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132 actataccat agtagtatag ctggtttagt tgatgccgag cagctcaacc tcgctaattg 3660
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138 <211> LENGTH: 1749
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149 1 5 10 15
150 gcc tca act cta gac acc agt aat acc cct acc atc aag aga gca gac 96
151 Ala Ser Thr Leu Asp Thr Ser Asn Thr Pro Thr Ile Lys Arg Ala Asp
152 20 25 30
153 gca gga aac aac acc tcc tca atc cca aca gcc acc ctc aac aac acc 144
154 Ala Gly Asn Asn Thr Ser Ser Ile Pro Thr Ala Thr Leu Asn Asn Thr
155 35 40 45
156 gtc ttc atc ggc cgt tcc ctg ccc gag ttc gag cag gag ttg ttc ctg 192
157 Val Phe Ile Gly Arg Ser Leu Pro Glu Phe Glu Gln Glu Leu Phe Leu
158 50 55 60
159 ggt atc aag ttt gct gat gag ccc gtg cga ttc acc ccg tcg acg ttg 240
160 Gly Ile Lys Phe Ala Asp Glu Pro Val Arg Phe Thr Pro Ser Thr Leu
161 65 70 75 80
162 aaa acc gtc tat cgc gcc aat gac agc gac aac ggg gtg tat cat gct 288
163 Lys Thr Val Tyr Arg Ala Asn Asp Ser Asp Asn Gly Val Tyr His Ala
164 85 90 95
165 tcc aca gca tcc gga ctg cag act tcc tcg ggg acc gtg ctc tac aac 336
166 Ser Thr Ala Ser Gly Leu Gln Thr Ser Ser Gly Thr Val Leu Tyr Asn
167 100 105 110
168 gcc aca gag tat ggg tat gat tgc ccc ggg tat gga tcc gat gag acg 384

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170			115					120					125				
171	gag	ctg	gcg	gag	gaa	gga	tat	gcg	cgg	ttc	gat	gag	aac	tgt	atg	aac	432
172	Glu	Leu	Ala	Glu	Glu	Gly	Tyr	Ala	Arg	Phe	Asp	Glu	Asn	Cys	Met	Asn	
173			130					135					140				
174	ctg	aat	ata	att	cgg	ccc	aag	aga	gag	aaa	gag	gat	gag	ttg	ttg	cct	480
175	Leu	Asn	Ile	Ile	Arg	Pro	Lys	Arg	Glu	Lys	Glu	Asp	Glu	Leu	Leu	Pro	
176	145					150					155				160		
177	gtg	atg	att	tgg	atc	ttt	ggt	ggt	ggt	tgg	gtg	cag	ggt	gcg	act	gct	528
178	Val	Met	Ile	Trp	Ile	Phe	Gly	Gly	Gly	Trp	Val	Gln	Gly	Ala	Thr	Ala	
179						165					170				175		
180	gat	ccg	agg	tac	aat	atg	agc	tat	att	ggt	cgc	cag	ggt	gcg	ttg	aat	576
181	Asp	Pro	Arg	Tyr	Asn	Met	Ser	Tyr	Ile	Val	Arg	Gln	Gly	Ala	Leu	Asn	
182				180						185				190			
183	gat	aag	cct	gtc	ttg	ggt	gtc	tgc	atc	aat	tac	cgt	gtg	gct	gcg	ttt	624
184	Asp	Lys	Pro	Val	Leu	Gly	Val	Ser	Ile	Asn	Tyr	Arg	Val	Ala	Ala	Phe	
185			195				200						205				
186	gga	ttc	ctt	gac	tct	gtc	gag	ggt	atg	gaa	tcc	ggc	aac	acg	aac	cta	672
187	Gly	Phe	Leu	Asp	Ser	Val	Glu	Val	Met	Glu	Ser	Gly	Asn	Thr	Asn	Leu	
188			210				215					220					
189	gga	ctt	cgt	gat	cag	cgc	gtc	gcc	atg	cat	tgg	gtc	aaa	caa	aac	atc	720
190	Gly	Leu	Arg	Asp	Gln	Arg	Val	Ala	Met	His	Trp	Val	Lys	Gln	Asn	Ile	
191	225					230					235				240		
192	aag	gcg	ttt	ggt	ggt	gac	ccg	gac	aag	atc	acc	atc	tgg	gga	gaa	tca	768
193	Lys	Ala	Phe	Gly	Gly	Asp	Pro	Asp	Lys	Ile	Thr	Ile	Trp	Gly	Glu	Ser	
194					245				250					255			
195	gct	ggt	gcc	tac	agc	gtc	gga	gcc	cac	ctg	gtc	acc	aac	gac	ggt	gac	816
196	Ala	Gly	Ala	Tyr	Ser	Val	Gly	Ala	His	Leu	Val	Thr	Asn	Asp	Gly	Asp	
197			260					265					270				
198	aac	gag	ggt	cta	ttc	aga	gcc	gcc	atc	atg	gaa	tcc	ggc	aac	gca	gtc	864
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202	Gly	Pro	Pro	Tyr	Asn	Gly	Thr	Asp	Trp	Tyr	Gln	Pro	Met	Tyr	Asp	Gln	
203			290				295					300					
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205	Ile	Val	Asn	Ala	Thr	Asn	Cys	Thr	Thr	Ser	Ser	Asn	Thr	Leu	Gln	Cys	
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207	ctc	cgc	gaa	gtc	ccc	ttc	tca	acg	atc	tac	acc	gcc	gca	gac	atc	ggc	1008
208	Leu	Arg	Glu	Val	Pro	Phe	Ser	Thr	Ile	Tyr	Thr	Ala	Ala	Asp	Ile	Gly	
209					325				330					335			
210	ctg	gaa	tgg	ttc	gcc	acc	atc	gac	ggc	acc	ttc	atc	aaa	gaa	tat	ccc	1056
211	Leu	Glu	Trp	Phe	Ala	Thr	Ile	Asp	Gly	Thr	Phe	Ile	Lys	Glu	Tyr	Pro	
212			340					345					350				
213	caa	atc	agc	att	acg	gag	ggc	cgc	ttc	gcc	aag	gtc	ccc	atc	ctc	cat	1104
214	Gln	Ile	Ser	Ile	Thr	Glu	Gly	Arg	Phe	Ala	Lys	Val	Pro	Ile	Leu	His	
215			355				360						365				
216	ggc	acc	aac	acc	gac	gag	ggc	gtg	agt	ttc	ggt	acg	acg	ggc	gtg	aac	1152
217	Gly	Thr	Asn	Thr	Asp	Glu	Gly	Val	Ser	Phe	Gly	Thr	Thr	Gly	Val	Asn	

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221 385      390      395      400
222 cta aac gaa acc caa gcc acg acc ctc cta tcg cac tat ccc aac atc      1248
223 Leu Asn Glu Thr Gln Ala Thr Thr Leu Leu Ser His Tyr Pro Asn Ile
224      405      410      415
225 tcc gcc cta ggc tgt ccc tac gga tgg ggc aac acg acc tgg ccg aag      1296
226 Ser Ala Leu Gly Cys Pro Tyr Gly Trp Gly Asn Thr Thr Trp Pro Lys
227      420      425      430
228 ctg ggg tat gaa tat aag cgc tac gag tcg atg gcg ggc gat ctg tgc      1344
229 Leu Gly Tyr Glu Tyr Lys Arg Tyr Glu Ser Met Ala Gly Asp Leu Cys
230      435      440      445
231 atg gtt gct ccg agg agg ttg ctc agt cag aag atg aag gag tat gag      1392
232 Met Val Ala Pro Arg Arg Leu Leu Ser Gln Lys Met Lys Glu Tyr Glu
233      450      455      460
234 gag caa gtg ttt gcg tat cgg tgg gat gtc gct gcg ttg aat gat tcg      1440
235 Glu Gln Val Phe Ala Tyr Arg Trp Asp Val Ala Leu Asn Asp Ser
236 465      470      475      480
237 agt acg att ggg gtg gcg cat ttt gct gag atc ccg ttt gtt ttc gcc      1488
238 Ser Thr Ile Gly Val Ala His Phe Ala Glu Ile Pro Phe Val Phe Ala
239      485      490      495
240 aac cct gtg cag aac atc act ccg ttg gga agt gat ccc gca aga ctg      1536
241 Asn Pro Val Gln Asn Ile Thr Pro Leu Gly Ser Asp Pro Ala Arg Leu
242      500      505      510
243 gag ttg ggt aat ctg gcc gcg agg atg tgg acg gct ttt gtg acg gat      1584
244 Glu Leu Gly Asn Leu Ala Ala Arg Met Trp Thr Ala Phe Val Thr Asp
245      515      520      525
246 ttg gat ccg aat ggg cat ggt gtc tct ggt atc ccc cac tgg ccg aaa      1632
247 Leu Asp Pro Asn Gly His Gly Val Ser Gly Ile Pro His Trp Pro Lys
248      530      535      540
249 tac aac ctc act gat ccg agg gac ttt gtg ttc ccg cta ccg agg gat      1680
250 Tyr Asn Leu Thr Asp Pro Arg Asp Phe Val Phe Arg Leu Pro Arg Asp
251 545      550      555      560
252 gga agt tat gtg gag aag gat act ttt agg acg ggg ggg att gat tat      1728
253 Gly Ser Tyr Val Glu Lys Asp Thr Phe Arg Thr Gly Gly Ile Asp Tyr
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VERIFICATION SUMMARY

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